



0400

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/825,244

Source: OIPE

Date Processed by STIC: 4-17-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/825,244

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**
- 8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) **(2) INFORMATION FOR SEQ ID NO:X:**
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) **<210> sequence id number**
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 ✓ Use of <220>Feature Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

DATE: 04/17/2001

PATENT APPLICATION: US/09/825,244

TIME: 10:43:09

Input Set : A:\0225-0033.24-SEQLIST.txt

Output Set: N:\CRF3\04172001\I825244.raw

Does Not Comply
Corrected Diskette Needed

p 1, 2, 3

4 <110> APPLICANT: Singh, Sharat
 5 Matray, Tracy
 6 Chenna, Ahmed
 8 <120> TITLE OF INVENTION: Sets of Generalized Target-Binding e-tag
 9 Probes
 11 <130> FILE REFERENCE: 0225-0033.24
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/825,244
 C--> 14 <141> CURRENT FILING DATE: 2001-04-02
 16 <150> PRIOR APPLICATION NUMBER: US 09/698,846
 17 <151> PRIOR FILING DATE: 2000-10-27
 19 <150> PRIOR APPLICATION NUMBER: US 09/684,386
 20 <151> PRIOR FILING DATE: 2000-10-04
 22 <150> PRIOR APPLICATION NUMBER: US 09/602,586
 23 <151> PRIOR FILING DATE: 2000-06-21
 25 <150> PRIOR APPLICATION NUMBER: US 09/561,579
 26 <151> PRIOR FILING DATE: 2000-04-28
 28 <150> PRIOR APPLICATION NUMBER: US 09/303,029
 29 <151> PRIOR FILING DATE: 1999-04-30
 31 <160> NUMBER OF SEQ ID NOS: 18
 33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 35 <210> SEQ ID NO 1
 36 <211> LENGTH: 16
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Artificial Sequence
 40 <220> FEATURE:
 41 <223> OTHER INFORMATION: oligonucleotide
 43 <400> SEQUENCE: 1
 44 tcaccacatc ccagtg
 46 <210> SEQ ID NO: 2
 47 <211> LENGTH: 16
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: oligonucleotide
 54 <400> SEQUENCE 2
 55 gagggaggtt tggttg
 57 <210> SEQ ID NO: 3
 58 <211> LENGTH: 22
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Artificial Sequence
 62 <220> FEATURE:
 63 <223> OTHER INFORMATION: oligonucleotide
 65 <221> NAME/KEY: misc_feature
 66 <222> LOCATION: (22)...(22)
 67 <223> OTHER INFORMATION: 3' nucleotide linked to tetramethyl rhodamine
 69 <400> SEQUENCE: 3
 70 ccagcaacca atgatgcccg tt

16

More specific explanation
 needed as to the source
 of the artificial sequences.
 oligonucleotide is too vague.
 See #12 on the Error Summary
 Sheet.

16

22

RAW SEQUENCE LISTING
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Input Set : A:\0225-0033.24-SEQLIST.txt
 Output Set: N:\CRF3\04172001\I825244.raw

72 <210> SEQ ID NO: 4
 73 <211> LENGTH: 22
 74 <212> TYPE: DNA
 75 <213> ORGANISM: Artificial Sequence
 77 <220> FEATURE:
 78 <223> OTHER INFORMATION: oligonucleotide → see p1
 80 <221> NAME/KEY: misc_feature
 81 <222> LOCATION: (1)...(1)
 82 <223> OTHER INFORMATION: 5' nucleotide linked to fluorescein
 84 <221> NAME/KEY: misc_feature
 85 <222> LOCATION: (22)...(22)
 86 <223> OTHER INFORMATION: 3' nucleotide linked to tetramethyl rhodamine
 88 <400> SEQUENCE: 4
 89 ccagcaagca ctgatgcctg tt 22
 91 <210> SEQ ID NO: 5
 92 <211> LENGTH: 4
 93 <212> TYPE: PRT
 94 <213> ORGANISM: Artificial Sequence
 96 <220> FEATURE:
 97 <223> OTHER INFORMATION: peptide linker
 99 <400> SEQUENCE: 5
 100 Lys Lys Ala Ala
 101 1
 103 <210> SEQ ID NO: 6
 104 <211> LENGTH: 4
 105 <212> TYPE: PRT
 106 <213> ORGANISM: Artificial Sequence
 108 <220> FEATURE:
 109 <223> OTHER INFORMATION: peptide linker
 111 <400> SEQUENCE: 6
 112 Lys Lys Lys Ala
 113 1
 115 <210> SEQ ID NO: 7
 116 <211> LENGTH: 4
 117 <212> TYPE: PRT
 118 <213> ORGANISM: Artificial Sequence
 120 <220> FEATURE:
 121 <223> OTHER INFORMATION: peptide linker
 123 <400> SEQUENCE: 7
 124 Lys Lys Lys Lys
 125 1
 127 <210> SEQ ID NO: 8
 128 <211> LENGTH: 25
 129 <212> TYPE: DNA
 130 <213> ORGANISM: Artificial Sequence
 132 <220> FEATURE:
 133 <223> OTHER INFORMATION: oligonucleotide → see p1
 135 <400> SEQUENCE: 8
 136 gaccaggaaa tagagaggaa atgta 25

RAW SEQUENCE LISTING DATE: 04/17/2001
 PATENT APPLICATION: US/09/825,244 TIME: 10:43:09

Input Set : A:\0225-0033.24-SEQLIST.txt
 Output Set: N:\CRF3\04172001\I825244.raw

138 <210> SEQ ID NO: 9
 139 <211> LENGTH: 27
 140 <212> TYPE: DNA
 141 <213> ORGANISM: Artificial Sequence
 143 <220> FEATURE:
 144 <223> OTHER INFORMATION: oligonucleotide
 146 <400> SEQUENCE: 9
 147 gaaggagaag gaagagttgg tattatc 27
 149 <210> SEQ ID NO: 10
 150 <211> LENGTH: 21
 151 <212> TYPE: DNA
 152 <213> ORGANISM: Artificial Sequence
 154 <220> FEATURE:
 155 <223> OTHER INFORMATION: oligonucleotide
 157 <400> SEQUENCE: 10
 158 ttgggctcag atctgtgata g 21
 160 <210> SEQ ID NO: 11
 161 <211> LENGTH: 27
 162 <212> TYPE: DNA
 163 <213> ORGANISM: Artificial Sequence
 165 <220> FEATURE:
 166 <223> OTHER INFORMATION: oligonucleotide
 168 <400> SEQUENCE: 11
 169 catctaggta tccaaaagga gagtcta 27
 171 <210> SEQ ID NO: 12
 172 <211> LENGTH: 27
 173 <212> TYPE: DNA
 174 <213> ORGANISM: Artificial Sequence
 176 <220> FEATURE:
 177 <223> OTHER INFORMATION: oligonucleotide
 179 <400> SEQUENCE: 12
 180 cagtatatag ttcttctca tgcatt 27
 182 <210> SEQ ID NO: 13
 183 <211> LENGTH: 20
 184 <212> TYPE: DNA
 185 <213> ORGANISM: Artificial Sequence
 187 <220> FEATURE:
 188 <223> OTHER INFORMATION: oligonucleotide
 190 <400> SEQUENCE: 13
 191 gcaagatctt cgccttactg 20
 193 <210> SEQ ID NO: 14
 194 <211> LENGTH: 32
 195 <212> TYPE: DNA
 196 <213> ORGANISM: Artificial Sequence
 198 <220> FEATURE:
 199 <223> OTHER INFORMATION: probe
 201 <221> NAME/KEY misc_feature
 202 <222> LOCATION: (1)...(1)
 203 <223> OTHER INFORMATION: e-tag10s modification to the 5' nucleotide

See p. 1

RAW SEQUENCE LISTING

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205 <400> SEQUENCE 14
206 ttccattttc tttttagagc agtatacaaa ga 32
208 <210> SEQ ID NO: 15
209 <211> LENGTH: 32
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: probe
216 <221> NAME/KEY: misc_feature
217 <222> LOCATION: (1)...(1)
218 <223> OTHER INFORMATION: e-tag10as modification to the 5' nucleotide
220 <400> SEQUENCE: 15
221 tctttgtata ctgctctaaa aagaaaatgg aa 32
223 <210> SEQ ID NO: 16
224 <211> LENGTH: 28
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: probe
231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: (1)...(1)
233 <223> OTHER INFORMATION: e-tag11s modification to the 5' nucleotide
235 <400> SEQUENCE: 16
236 aaactccagc atagatgtgg atagcttg 28
238 <210> SEQ ID NO: 17
239 <211> LENGTH: 28
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: probe
246 <221> NAME/KEY: misc_feature
247 <222> LOCATION: (1)...(1)
248 <223> OTHER INFORMATION: (e-tag11as)modification to the 5' nucleotide
250 <400> SEQUENCE: 17
251 caagctatcc acatctatgc tggagttt 28
253 <210> SEQ ID NO: 18
254 <211> LENGTH: 23
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: probe
261 <221> NAME/KEY: misc_feature
262 <222> LOCATION: (1)...(1)
263 <223> OTHER INFORMATION: e-tag13as modification to the 5' nucleotide
265 <400> SEQUENCE: 18
266 aactgcttgt ggccatggct tag 23

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VERIFICATION SUMMARY

DATE: 04/17/2001

PATENT APPLICATION: US/09/825,244

TIME: 10:43:10

Input Set : A:\0225-0033.24-SEQLIST.txt

Output Set: N:\CRF3\04172001\I825244.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date